! FINDPATTERNS on geneseqp: allowing 0 mismatches

! 1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L) May

AAW32305 ck: 992 len: 542 ! Aaw32305 Arabidopsis thaliana inorganic phc
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(L)xFx(R)(F)Wxx(F)
130: GVMAT LCFFRFWLGF GIGGD

AAW32302 ck: 605 len: 534 ! Aaw32302 Arabidopsis thaliana inorganic phc
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(L)xFx(R)(F)Wxx(F)
130: AVMAT LCFFRFWLGF GIGGD

AAW32303 ck: 4821 len: 521 ! Aaw32303 Arabidopsis thaliana inorganic phc
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(L)xFx(R)(F)Wxx(F)
130: GVMTT LCFFRFWLGF GIGGD

AAW32304 ck: 8027 len: 524 ! Aaw32304 Arabidopsis thaliana inorganic phc
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(L)xFx(R)(F)Wxx(F)
130: GVMTT LCFFRFWLGF GIGGD

AAW32301 ck: 8746 len: 524 ! Aaw32301 Arabidopsis thaliana inorganic phc
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(L)xFx(R)(F)Wxx(F)
130: GVMTT LCFFRFWLGF GIGGD

AAW30486 ck: 8893 len: 135 ! Aaw30486 Flea saliva protein fspN (PfspN6-1
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(P)xFx(R)(F)Wxx(Q)
108: HFDAM PGFSRFWNPQ QCPAY

AAW36137 ck: 605 len: 534 ! Aaw36137 A. thaliana inorganic phosphate tr
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(L)xFx(R)(F)Wxx(F)
130: AVMAT LCFFRFWLGF GIGGD

AAW82377 ck: 8893 len: 135 ! Aaw82377 Flea saliva protein PfspN6-135. 4
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(P)xFx(R)(F)Wxx(Q)
108: HFDAM PGFSRFWNPQ QCPAY

AAW82382 ck: 6654 len: 375 ! Aaw82382 Flea saliva protein PfspN6-375. 4
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(P)xFx(R)(F)Wxx(Q)
134: HFDAM PGFSRFWNPQ QCPAY

AAW82384 ck: 2624 len: 356 ! Aaw82384 Flea saliva protein PfspN6-356. 4
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(P)xFx(R)(F)Wxx(Q)
115: HFDAM PGFSRFWNPQ QCPAY

AAW82385 ck: 309 len: 355 ! Aaw82385 Flea saliva protein PfspN6-357.
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(P)xFx(R)(F)Wxx(Q)
114: HFDAM PGFSRFWNPQ QCPAY

AAW82322 ck: 4400 len: 19 ! Aaw82322 p53 homologue TIP 12/1 peptide.
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(P)xFx(D)(Y)Wxx(L)
6: PPLSM PRFMDYWEGL NENG

AAW82320 ck: 4400 len: 19 ! Aaw82320 p53 homologue TIP 12/1 peptide.
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(P)xFx(D)(Y)Wxx(L)
6: PPLSM PRFMDYWEGL NENG

AAW58852 ck: 5772 len: 130 ! Aaw58852 Human O289_1 secreted protein.
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(C)xFx(S)(F)Wxx(L)
119: VISHL CHFSSFWIGL PA

AAW56025 ck: 9188 len: 316 ! Aaw56025 Phosphate starvation-induced pr
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(L)xFx(R)(F)Wxx(F)
31: SVMTT LCFFRFWLGF GIGGD

AAW37220 ck: 5978 len: 12 ! Aaw37220 MDM2 binding peptide unique pha
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(P)xFx(D)(Y)Wxx(L)
2: M PRFMDYWEGL N

AAW37224 ck: 9428 len: 15 ! Aaw37224 MDM2 binding peptide unique pha
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(L)xFx(D)(Y)Wxx(L)
5: PRPA LVFADYWETL Y

AAW37221 ck: 6151 len: 12 ! Aaw37221 MDM2 binding peptide unique pha
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(Q)xFx(D)(Y)Wxx(Q)
2: V QNFIDYWTQQ F

AAW37222 ck: 5993 len: 12 ! Aaw37222 MDM2 binding peptide unique pha
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(P)xFx(H)(Y)Wxx(F)
3: TG PAFTHYWATF

AAW37223 ck: 9093 len: 15 ! Aaw37223 MDM2 binding peptide unique pha
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)
(P)xFx(D)(H)Wxx(L)
5: IDRA PTFRDHWFAL V

AAW37225 ck: 8833 len: 15 ! Aaw37225 MDM2 binding peptide unique pha

```
=> fil reg; d que 13
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TSCA INFORMATION NOW CURRENT THROUGH July 7, 2001

  Please note that search-term pricing does apply when
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Crossover limits have been increased.  See HELP CROSSOVER for details.

Calculated physical property data is now available.  See HELP PROPERTIES
for more information.  See STNote 27, Searching Properties in the CAS
Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

L2          259 SEA FILE=REGISTRY ABB=ON  [PLECQ].F.[RHECSD][HFY]W..[FQL]/SQSP
L3            2 SEA FILE=REGISTRY ABB=ON  L2 AND SQL<11
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sequence length less than 11

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=> d rn cn kwic nte 13 1-2; fil capl; d que 14
L3   ANSWER 1 OF 2  REGISTRY  COPYRIGHT 2002 ACS
RN   393113-23-0 REGISTRY
CN   L-Leucine, L-prolyl-L-arginyl-L-phenylalanyl-L-methionyl-L-.alpha.-
     aspartyl-L-tyrosyl-L-tryptophyl-L-.alpha.-glutamylglycyl- (9CI)  (CA INDEX
     NAME)
SQL  10

SEQ      1 PRFMDYWEGL
           ==========
HITS AT:  1-10

L3   ANSWER 2 OF 2  REGISTRY  COPYRIGHT 2002 ACS
RN   267004-47-7  REGISTRY
CN   Peptide, (Pro-Xaa-Phe-Xaa-Asp-Tyr-Trp-Xaa-Xaa-Leu) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   109: PN: WO0024782 SEQID: 142 claimed protein
CN   727: PN: WO0183525 TABLE: 13 claimed protein
SQL  10

SEQ      1 PXFXDYWXXL
           ==========
HITS AT:  1-10
NTE
```

type	location		description
uncommon	Aaa-2	-	-
uncommon	Aaa-4	-	-
uncommon	Aaa-8	-	-
uncommon	Aaa-9	-	-

use Registry # to match sequence to citation

sequence length = SQL

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L2            259 SEA FILE=REGISTRY ABB=ON  [PLECQ].F.[RHECSD][HFY]W..[FQL]/SQSP
L3              2 SEA FILE=REGISTRY ABB=ON  L2 AND SQL<11
L4              3 SEA FILE=CAPLUS ABB=ON  L3
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=> d ibib ab hitrn l4 1-3

L4 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:829830 CAPLUS
DOCUMENT NUMBER: 136:128583
TITLE: QSAR: hydropathic analysis of inhibitors of the p53-mdm2 interaction
AUTHOR(S): Galatin, Peter S.; Abraham, Donald J.
CORPORATE SOURCE: Department of Medicinal Chemistry and Institute for Structural Biology and Drug Discovery, Virginia Commonwealth University, Richmond, VA, 23298, USA
SOURCE: Proteins: Structure, Function, and Genetics (2001), 45(3), 169-175
CODEN: PSFGEY; ISSN: 0887-3585
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB To date, a no. of p53-derived peptides have been evaluated in vitro for their ability to inhibit the carcinogenic p53-mdm2 interaction. Design of second-generation nonpeptidic compds. requires the redn. of large peptide structures down to small mols. maintaining the proper spatial arrangement of key functional groups. Mol. modeling software exists that can predict and rank intermol. interactions from the p53-mdm2 complex crystal structure. Such analyses can yield a pharmacophore model suitable as a search query for a 3D chem. database to generate new lead compds. As preliminary validation of this methodol., the Hydropathic INTeractions (HINT) program has been used to generate noncovalent interaction measurements between reported peptide inhibitors and mdm2. Quant. structure-activity relationships were developed expressing peptide